SEQ SEARCH SUMMARY

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 04:07:44 ; Search time 4678 Seconds
                                          (without alignments)
                                          11220.268 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY NUC
                Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   GenEmbl:*
            1:   gb_ba:*
            2:   gb_htg:*
            3:   gb_in:*
            4:   gb_om:*
            5:   gb_ov:*
            6:   gb_pat:*
            7:   gb_ph:*
            8:   gb_pl:*
            9:   gb_pr:*
            10: gb_ro:*
            11: gb_sts:*
            12: gb_sy:*
            13: gb_un:*
            14: gb_vi:*
            15: em_ba:*
            16: em_fun:*
            17: em_hum:*
            18: em_in:*
            19: em_mu:*
            20: em_om:*
            21: em_or:*
            22: em_ov:*
            23: em_pat:*
            24: em_ph:*
            25: em_pl:*
            26: em_ro:*
            27: em_sts:*

```
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Applicant's

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1211	100.0	1211	6	AX394331	WO 02/18599	AX394331 Sequence
2	1211	100.0	309400	6	AX127153	EP 1108770	AX127153 Sequence
3	1211	100.0	325651	1	AP005283	GenBank	AP005283 Corynebac
4	603	49.8	603	6	AX123500		AX123500 Sequence
5	603	49.8	603	6	BD165617		BD165617 Novel pol
c 6	449	37.1	1185	6	AX123502		AX123502 Sequence
c 7	449	37.1	1185	6	BD165619		BD165619 Novel pol
8	243.6	20.1	87340	1	AP005224		AP005224 Corynebac
9	197	16.3	951	6	AX123501		AX123501 Sequence
10	197	16.3	951	6	BD165618		BD165618 Novel pol
11	194.8	16.1	53793	1	BX248361		BX248361 Corynebac
12	96.8	8.0	1775	1	AF023161		AF023161 Mycobacte
13	82	6.8	210205	1	AY223810		AY223810 Rhodococc
c 14	79.6	6.6	1443	6	AR227225		AR227225 Sequence
15	79.6	6.6	302988	1	AE017176		AE017176 Porphyrom
16	79	6.5	1800	1	MLTRTRXHP		X87899 M.leprae TR
17	79	6.5	40571	1	MSGDNAB		L39923 Mycobacteri
18	79	6.5	269203	1	MLEPRTN10		AL583926 Mycobacte
19	78	6.4	3457	6	AX764249		AX764249 Sequence
20	78	6.4	3457	6	AX773631		AX773631 Sequence
21	77.6	6.4	300956	1	AE016963		AE016963 Coxiella
22	75	6.2	1529	1	MTTRTRXGN		X95798 M.tuberculo
23	75	6.2	9882	1	AE007194		AE007194 Mycobacte
24	75	6.2	10940	1	AE009169		AE009169 Agrobacte
25	75	6.2	12357	1	AE008135		AE008135 Agrobacte
c 26	75	6.2	35336	1	MSGY367		AD000008 Mycobacte
27	75	6.2	244800	1	BX842584		BX842584 Mycobacte
28	73.4	6.1	278492	1	BX248347		BX248347 Mycobacte
c 29	72.8	6.0	7542	1	CBTRXB		X75627 C.burnetii
c 30	72.6	6.0	49617	6	AR408749		AR408749 Sequence
c 31	72.6	6.0	49617	6	AX067453		AX067453 Sequence
32	71.8	5.9	2556	1	AF009622		AF009622 Listeria
c 33	71.8	5.9	324050	1	AL591983		AL591983 Listeria

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 04:06:14 ; Search time 503 Seconds
                                          (without alignments)
                                          10227.769 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID		Description
1	1211	100.0	1211	6	AAL42355	WO 02/18577	Aal42355 Corynebac
2	1211	100.0	309400	5	AAH68534	EP 1108770	Aah68534 C glutami
3	603	49.8	603	5	AAH68381		Aah68381 C glutami
4	603	49.8	603	7	ACA01297		Aca01297 C. glutam
c 5	449	37.1	1185	5	AAH68383		Aah68383 C glutami
6	197	16.3	951	5	AAH68382		Aah68382 C glutami
7	197	16.3	951	7	ACA01298		Aca01298 C. glutam
8	79	6.5	1377	6	ABN89593		Abn89593 Mycobacte

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 05:05:10 ; Search time 113 Seconds
                                          (without alignments)
                                          5947.306 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
 c   1   79.6   6.6   1443   4   US-09-221-017B-685   Sequence 685, App
      2   75   6.2 4403765 3   US-09-103-840A-2   Sequence 2, Appli
      3   75   6.2 4411529 3   US-09-103-840A-1   Sequence 1, Appli
 c   4   72.6   6.0 49617   4   US-09-596-002-28   Sequence 28, Appl
      5   69.4   5.7   1020   4   US-09-543-681A-1461   Sequence 1461, Ap
      6   63.6   5.3   933   4   US-09-134-000C-2109   Sequence 2109, Ap
      7   63.2   5.2   600   4   US-09-252-991A-14870   Sequence 14870, A
 c   8   63.2   5.2   666   4   US-09-252-991A-14492   Sequence 14492, A
      9   62.6   5.2   972   4   US-09-252-991A-13278   Sequence 13278, A
 c   10   62.6   5.2   1413   4   US-09-252-991A-12680   Sequence 12680, A
     11   61.8   5.1   1050   4   US-09-489-039A-4925   Sequence 4925, Ap
     12   61.2   5.1   264   4   US-09-134-001C-2660   Sequence 2660, Ap

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 06:38:32 ; Search time 531 Seconds
                                          (without alignments)
                                          10316.224 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   Published_Applications_NA:*
          1:   /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
          2:   /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
          3:   /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
          4:   /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
          5:   /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
          6:   /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
          7:   /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
          8:   /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
          9:   /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
          10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
          11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
          12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
          13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
          14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
          15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
          16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
          17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
          18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
          19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1211	100.0	1211	9	US-09-942-935-1	Sequence 1, Appli
	2	1211	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
	3	603	49.8	603	9	US-09-738-626-3416	Sequence 3416, Ap
c	4	449	37.1	1185	9	US-09-738-626-3418	Sequence 3418, Ap
	5	197	16.3	951	9	US-09-738-626-3417	Sequence 3417, Ap
c	6	79.6	6.6	1443	13	US-10-194-163-685	Sequence 685, App
	7	79	6.5	1377	15	US-10-032-201B-50	Sequence 50, Appl
	8	79	6.5	4922	15	US-10-032-201B-30	Sequence 30, Appl
c	9	72.6	6.0	49617	13	US-10-672-787-28	Sequence 28, Appl
c	10	68.6	5.7	977	16	US-10-398-221-3269	Sequence 3269, Ap
c	11	63.6	5.3	5998	9	US-09-070-927A-119	Sequence 119, App
	12	62.2	5.1	311	9	US-09-974-300-6285	Sequence 6285, Ap
	13	60.8	5.0	1608	9	US-09-938-842A-2322	Sequence 2322, Ap
	14	60.8	5.0	1608	11	US-09-938-842A-2322	Sequence 2322, Ap
	15	60.4	5.0	969	15	US-10-156-761-4289	Sequence 4289, Ap
	16	60.4	5.0	9025608	15	US-10-156-761-1	Sequence 1, Appli
	17	60.2	5.0	966	15	US-10-091-841-27	Sequence 27, Appl
	18	60.2	5.0	966	15	US-10-032-201B-44	Sequence 44, Appl
	19	58.8	4.9	684707	16	US-10-398-221-9	Sequence 9, Appli
c	20	58.8	4.9	3011208	16	US-10-398-221-2058	Sequence 2058, Ap
	21	56.4	4.7	936	9	US-09-925-637-13	Sequence 13, Appl
	22	56.4	4.7	936	15	US-10-084-205-13	Sequence 13, Appl
	23	56.4	4.7	13086	8	US-08-781-986A-16	Sequence 16, Appl
	24	56.4	4.7	13086	13	US-10-329-624-16	Sequence 16, Appl
	25	55	4.5	711	15	US-10-156-761-4287	Sequence 4287, Ap
c	26	55	4.5	1286	11	US-09-764-875-63	Sequence 63, Appl
c	27	51.8	4.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
c	28	51.8	4.3	1830121	16	US-10-329-670-1	Sequence 1, Appli
	29	51.2	4.2	19024	9	US-09-070-927A-179	Sequence 179, App
	30	51.2	4.2	640681	9	US-09-790-988-1	Sequence 1, Appli
	31	50.6	4.2	1021	15	US-10-306-292-24	Sequence 24, Appl
	32	49.2	4.1	1286	13	US-10-425-114-5073	Sequence 5073, Ap
	33	49.2	4.1	1325	13	US-10-425-114-3716	Sequence 3716, Ap
	34	48	4.0	3249	9	US-09-738-626-3414	Sequence 3414, Ap
	35	47.4	3.9	995	15	US-10-091-841-10	Sequence 10, Appl
	36	47.4	3.9	995	15	US-10-091-841-23	Sequence 23, Appl
	37	45.4	3.7	579	9	US-09-738-626-284	Sequence 284, App
	38	45.4	3.7	1109	9	US-09-941-936A-1	Sequence 1, Appli
	39	45.4	3.7	1284	13	US-10-425-114-29681	Sequence 29681, A
	40	45.4	3.7	1645	13	US-10-424-599-65583	Sequence 65583, A
c	41	45.4	3.7	3309400	9	US-09-738-626-1	Sequence 1, Appli
	42	44.8	3.7	1047	16	US-10-320-797-2136	Sequence 2136, Ap
	43	43.8	3.6	1403	16	US-10-320-797-1136	Sequence 1136, Ap
	44	43.8	3.6	3403	16	US-10-320-797-136	Sequence 136, App
	45	43	3.6	1560	15	US-10-306-292-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-942-935-1

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 05:02:41 ; Search time 2986 Seconds
                                          (without alignments)
                                          12110.884 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*
                 28: gb_gss1:*

```
                29:  gb_gss2:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                  SUMMARIES
                        %
      Result           Query
        No.    Score  Match Length DB   ID                   Description
      ------------------------------------------------------------------------
          1    75.2    6.2    643   14  CF418809             CF418809 USDA-FP_1
          2    75.2    6.2    682   14  CF418521             CF418521 USDA-FP_1
          3    75.2    6.2    690   14  CF418413             CF418413 USDA-FP_1
          4    75.2    6.2    789   14  CD576244             CD576244 UCRPT01_0
          5    72.4    6.0    646   12  BI096251             BI096251 S1D_F05_S
          6    72.2    6.0    535    9  AV628023           AV628023 AV628023
          7    71.2    5.9    389   14  CF608768             CF608768 GERMO01_0
          8    68.6    5.7    721   13  BQ862556             BQ862556 QGC21G18.
          9    67.4    5.6    755   13  BQ863331             BQ863331 QGC23J12.
         10    64.4    5.3    483   13  BQ595059             BQ595059 E012711-0
         11      63    5.2    623   14  CA839585             CA839585 MCT029B08
         12      63    5.2    664   14  CA840153             CA840153 MCT040C12
         13    62.4    5.2    494   14  CB264406             CB264406 65-E01465
         14      61    5.0    490   10  BE321389             BE321389 NF024C10I
         15      61    5.0    523   10  BE321441             BE321441 NF025C10I
         16      61    5.0    593   12  BG452377             BG452377 NF085C09L
         17      61    5.0    609   12  BG451523             BG451523 NF110B04D
         18      61    5.0    655   10  BF650364             BF650364 NF096A12E
         19      61    5.0    659   10  BF636499             BF636499 NF091G04D
         20      61    5.0    662   10  BE322274             BE322274 NF022E01I
         21      61    5.0    663   10  AW692011             AW692011 NF046F03S
         22      61    5.0    666   13  BQ139032             BQ139032 NF010C06P
         23      61    5.0    667   13  BQ138990             BQ138990 NF009H09P
         24      61    5.0    671   12  BG449209             BG449209 NF043G10I
         25      61    5.0    683   14  CF068230             CF068230 EST668951
         26      61    5.0    692   10  BF520046             BF520046 EST457514
         27      61    5.0    949   14  CK291588             CK291588 EST754302
         28    60.8    5.0    563    9  AW030413           AW030413 EST273668
         29    60.8    5.0    564   10  BE449605             BE449605 EST356364
         30    60.8    5.0    590    9  AV828748           AV828748 AV828748
         31    60.2    5.0    592   12  BJ073890             BJ073890 BJ073890
         32      60    5.0    504   10  BE321909             BE321909 NF045F02I
      c  33      60    5.0    571   10  AW650215             AW650215 EST328669
         34    59.2    4.9    345   10  BE920457             BE920457 EST424226
         35    59.2    4.9    521   12  BG589427             BG589427 EST497269
         36    59.2    4.9    531   10  BE920949             BE920949 EST424718
         37    59.2    4.9    756   12  BG600533             BG600533 EST505428
         38    59.2    4.9    869   14  CK250778             CK250778 EST734415
         39    59.2    4.9    895   14  CK251220             CK251220 EST734857
         40    59.2    4.9    948   14  CK258509             CK258509 EST742146
         41    59.2    4.9    952   14  CK257230             CK257230 EST740867
         42    59.2    4.9    982   14  CK246570             CK246570 EST730207
         43      59    4.9    582   14  CA655448             CA655448 wlm0.pk00
         44    57.8    4.8    615   12  BQ045955             BQ045955 EST595073
         45    57.2    4.7    240    9  AV628019           AV628019 AV628019
```

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                         GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:          May  1, 2004, 07:30:51 ; Search time 4676 Seconds
                                          (without alignments)
                                          11225.067 Million cell updates/sec

Title:           US-09-942-935-1
Perfect score:   1211
Sequence:        1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table:   OLIGO NUC
                 Gapop 60.0 , Gapext 60.0

Searched:        3470272 seqs, 21671516995 residues

Word size :      0

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       GenEmbl:*
                 1:  gb_ba:*
                 2:  gb_htg:*
                 3:  gb_in:*
                 4:  gb_om:*
                 5:  gb_ov:*
                 6:  gb_pat:*
                 7:  gb_ph:*
                 8:  gb_pl:*
                 9:  gb_pr:*
                 10: gb_ro:*
                 11: gb_sts:*
                 12: gb_sy:*
                 13: gb_un:*
                 14: gb_vi:*
                 15: em_ba:*
                 16: em_fun:*
                 17: em_hum:*
                 18: em_in:*
                 19: em_mu:*
                 20: em_om:*
                 21: em_or:*
                 22: em_ov:*
                 23: em_pat:*
                 24: em_ph:*
                 25: em_pl:*
                 26: em_ro:*
                 27: em_sts:*
```

```
28:   em_un:*
29:   em_vi:*
30:   em_htg_hum:*
31:   em_htg_inv:*
32:   em_htg_other:*
33:   em_htg_mus:*
34:   em_htg_pln:*
35:   em_htg_rod:*
36:   em_htg_mam:*
37:   em_htg_vrt:*
38:   em_sy:*
39:   em_htgo_hum:*
40:   em_htgo_mus:*
41:   em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1211	100.0	1211	6	AX394331 *WO 02/18579*	AX394331 Sequence
2	1211	100.0	309400	6	AX127153 *EP*	AX127153 Sequence
3	1211	100.0	325651	1	AP005283 — *GenBank*	AP005283 Corynebac
4	603	49.8	603	6	AX123500 *EP*	AX123500 Sequence
5	603	49.8	603	6	BD165617 *JP*	BD165617 Novel pol
c 6	449	37.1	1185	6	AX123502 *EP*	AX123502 Sequence
c 7	449	37.1	1185	6	BD165619 *JP*	BD165619 Novel pol
8	197	16.3	951	6	AX123501 *EP*	AX123501 Sequence
9	197	16.3	951	6	BD165618 *JP*	BD165618 Novel pol
10	78	6.4	3457	6	AX764249 *WO 03/40681*	AX764249 Sequence
11	78	6.4	3457	6	AX773631 *WO 03/46123*	AX773631 Sequence
12	71	5.9	3075	6	AX064225 *WO 01/00843* —	AX064225 Sequence — *Seq:507*
13	71	5.9	3075	6	AX064311 "	AX064311 Sequence : *543*
14	48	4.0	3249	6	AX123498 *EP*	AX123498 Sequence
15	48	4.0	3249	6	BD165615 *JP*	BD165615 Novel pol
c 16	22	1.8	191712	2	BX323582	BX323582 Danio rer
c 17	21	1.7	3506	6	AX319470	AX319470 Sequence
18	21	1.7	144699	2	AC125881	AC125881 Rattus no
c 19	21	1.7	153841	2	AC091527	AC091527 Trypanoso
20	21	1.7	157848	10	AC091712	AC091712 Rattus no
21	21	1.7	168843	2	AC091711	AC091711 Rattus no
c 22	21	1.7	196904	2	AC113217	AC113217 Rattus no
c 23	21	1.7	211624	10	AC114817	AC114817 Mus muscu
24	21	1.7	242400	2	AC096829	AC096829 Rattus no
25	21	1.7	247946	2	AC133092	AC133092 Mus muscu
26	21	1.7	252376	2	AC105580	AC105580 Rattus no
27	20	1.7	1302	6	AX413806	AX413806 Sequence
28	20	1.7	2734	8	ARU421692	AJ421692 Anaptychi
c 29	20	1.7	3010	1	AF105341	AF105341 Listeria
c 30	20	1.7	37533	3	CBRG36C02	AC084560 Caenorhab
c 31	20	1.7	75650	2	AC018145	AC018145 Drosophil
32	20	1.7	77157	8	AP004114	AP004114 Oryza sat
33	20	1.7	87340	1	AP005224	AP005224 Corynebac

Pompejus

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 07:28:32 ; Search time 505 Seconds
                                           (without alignments)
                                           10187.263 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211
Scoring table: OLIGO_NUC
                Gapop 60.0 , Gapext 60.0
Searched: 3373863 seqs, 2124099041 residues
Word size :   0
Total number of hits satisfying chosen parameters: 6747726
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Listing first 45 summaries

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                SUMMARIES

          %
Result   Query
   No.   Score Match Length DB ID   Description
----
     1   1211 100.0   1211 6 AAL42355 ωo-18599   Aal42355 Corynebac
     2   1211 100.0 309400 5 AAH68534 EP   Aah68534 C glutami
     3   603   49.8   603 5 AAH68381 EP   Aah68381 C glutami
     4   603   49.8   603 7 ACA01297 DE 10128510   Aca01297 C. glutam
  c 5   449   37.1   1185 5 AAH68383 EP   Aah68383 C glutami
     6   197   16.3   951 5 AAH68382 EP   Aah68382 C glutami
     7   197   16.3   951 7 ACA01298 DE   Aca01298 C. glutam
     8   78   6.4   3457 9 ADD13494 ωo 03/40681   Add13494 C. glutam
     9   71   5.9   3075 4 AAF72006 ωo 01/00843   Aaf72006 Corynebac
    10   71   5.9   3075 4 AAF72049   "   Aaf72049 Corynebac
    11   48   4.0   3249 5 AAH68379 EP   Aah68379 C glutami
  c 12   21   1.7   3506 6 AAI64198 ωo 01/83563   Aai64198 Rat CRF2a
  c 13   21   1.7   5011 9 ADD31993 ∞ 03/110521 US   Add31993 Rat corti
    14   20   1.7   28 6 AAL42358   Aal42358 Corynebac
  c 15   20   1.7   28 6 AAL42359   Aal42359 Corynebac

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OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 08:35:47 ; Search time 114 Seconds
                                          (without alignments)
                                          5895.136 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_NA:*
                 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                        %
Result   Query
    No.   Score   Match Length DB   ID   Description
----
 c   1   19   1.6   963 4   US-09-252-991A-2989   Sequence 2989, Ap
     2   19   1.6   1431 4   US-09-252-991A-2787   Sequence 2787, Ap
 c   3   19   1.6   1707 4   US-09-252-991A-3180   Sequence 3180, Ap
 c   4   19   1.6   1709 4   US-08-936-165A-188   Sequence 188, App
     5   18   1.5   2069 1   US-07-921-178A-1   Sequence 1, Appli
 c   6   18   1.5 1230025 4   US-09-198-452A-1   Sequence 1, Appli
 c   7   17   1.4   404 2   US-08-951-648-33   Sequence 33, Appl
 c   8   17   1.4   404 3   US-09-174-437-33   Sequence 33, Appl
 c   9   17   1.4   404 4   US-09-686-055A-33   Sequence 33, Appl
    10   17   1.4   453 4   US-09-543-681A-3969   Sequence 3969, Ap
    11   17   1.4   495 4   US-09-252-991A-15616   Sequence 15616, A
 c 12   17   1.4   528 2   US-08-687-080-83   Sequence 83, Appl

```
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OM nucleic - nucleic search, using sw model

Run on:           May  1, 2004, 10:11:48 ; Search time 532 Seconds
                                          (without alignments)
                                          10296.833 Million cell updates/sec


Title:            US-09-942-935-1
Perfect score:    1211
Sequence:         1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211


Scoring table:    OLIGO_NUC
                  Gapop 60.0 , Gapext 60.0


Searched:         2936184 seqs, 2261732022 residues


Word size :       0


Total number of hits satisfying chosen parameters:      5872368


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Listing first 45 summaries


Database :        Published_Applications_NA:*
                  1:  /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                  2:  /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                  3:  /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                  4:  /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                  5:  /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                  6:  /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                  7:  /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                  8:  /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                  9:  /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                  10:  /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                  11:  /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
                  12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
                  13:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
                  14:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
                  15:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
                  16:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
                  17:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
                  18:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
                  19:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.
```

```
                            SUMMARIES              Nakagawa
                         %
        Result          Query
          No.   Score  Match Length DB   ID                        Description
        --------------------------------------------------------------------------------
            1    1211  100.0   1211  9   US-09-942-935-1           Sequence 1, Appli
            2    1211  100.0 3309400  9   US-09-738-626-1           Sequence 1, Appli
            3     603   49.8    603  9   US-09-738-626-3416        Sequence 3416, Ap
    c       4     449   37.1   1185  9   US-09-738-626-3418        Sequence 3418, Ap
            5     197   16.3    951  9   US-09-738-626-3417        Sequence 3417, Ap
            6      48    4.0   3249  9   US-09-738-626-3414        Sequence 3414, Ap
    c       7      21    1.7   3506  9   US-09-847-852-1           Sequence 1, Appli
    c       8      21    1.7   5011 15   US-10-293-702-1           Sequence 1, Appli
            9      20    1.7   1302 16   US-10-398-221-797         Sequence 797, App
    c      10      19    1.6    300 15   US-10-156-761-1964        Sequence 1964, Ap
    c      11      19    1.6   1709  9   US-09-939-980-188         Sequence 188, App
           12      19    1.6   3062 13   US-10-282-122A-31528      Sequence 31528, A
           13      19    1.6   6378 15   US-10-311-455-149         Sequence 149, App
           14      19    1.6 9025608 15   US-10-156-761-1           Sequence 1, Appli
    c      15      18    1.5    434 13   US-10-027-632-86208       Sequence 86208, A
    c      16      18    1.5    434 13   US-10-027-632-178940      Sequence 178940,
    c      17      18    1.5    434 16   US-10-027-632-86208       Sequence 86208, A
    c      18      18    1.5    434 16   US-10-027-632-178940      Sequence 178940,
    c      19      18    1.5    567 15   US-10-156-761-5054        Sequence 5054, Ap
    c      20      18    1.5    648 13   US-10-027-632-8947        Sequence 8947, Ap
    c      21      18    1.5    648 16   US-10-027-632-8947        Sequence 8947, Ap
    c      22      18    1.5    678 13   US-10-027-632-273855      Sequence 273855,
    c      23      18    1.5    678 16   US-10-027-632-273855      Sequence 273855,
           24      18    1.5    749 13   US-10-027-632-11318       Sequence 11318, A
           25      18    1.5    749 13   US-10-027-632-11319       Sequence 11319, A
           26      18    1.5    749 16   US-10-027-632-11318       Sequence 11318, A
           27      18    1.5    749 16   US-10-027-632-11319       Sequence 11319, A
           28      18    1.5   1590 16   US-10-369-493-37601       Sequence 37601, A
           29      18    1.5   1914 16   US-10-369-493-28918       Sequence 28918, A
    c      30      18    1.5   2000  9   US-09-887-576-852         Sequence 852, App
           31      18    1.5   2069 12   US-10-152-319A-1639       Sequence 1639, Ap
           32      18    1.5   4383 16   US-10-369-493-46057       Sequence 46057, A
    c      33      18    1.5   6170 13   US-10-363-616-184         Sequence 184, App
    c      34      18    1.5  10907 16   US-10-429-802-31          Sequence 31, Appl
    c      35      18    1.5  10907 16   US-10-430-503-22          Sequence 22, Appl
    c      36      18    1.5  11460 13   US-10-415-058-7           Sequence 7, Appli
           37      18    1.5  69300 13   US-10-415-058-6           Sequence 6, Appli
    c      38      18    1.5  91552 13   US-10-415-058-5           Sequence 5, Appli
    c      39      18    1.5 119596 15   US-10-270-336-3           Sequence 3, Appli
           40      18    1.5 185555 13   US-10-087-192-1999        Sequence 1999, Ap
           41      18    1.5 653122 13   US-10-087-192-226         Sequence 226, App
    c      42      18    1.5 1230025 16   US-10-289-762-1           Sequence 1, Appli
    c      43      17    1.4    116  9   US-09-966-880A-14         Sequence 14, Appl
    c      44      17    1.4    120  9   US-09-969-373-1351        Sequence 1351, Ap
           45      17    1.4    173  9   US-09-864-761-26899       Sequence 26899, A
```

                              ALIGNMENTS

RESULT 1
US-09-942-935-1

OM nucleic - nucleic search, using sw model

Run on: May 1, 2004, 08:33:17 ; Search time 2985 Seconds
                                         (without alignments)
                                         12114.942 Million cell updates/sec

Title: US-09-942-935-1
Perfect score: 1211
Sequence: 1 gacaccaatccacagatgca..........ccaggctttgaaaagggaat 1211

Scoring table: OLIGO_NUC
                 Gapop 60.0 , Gapext 60.0

Searched: 27513289 seqs, 14931090276 residues

Word size :   0

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   EST:*
                 1: em_estba:*
                 2: em_esthum:*
                 3: em_estin:*
                 4: em_estmu:*
                 5: em_estov:*
                 6: em_estpl:*
                 7: em_estro:*
                 8: em_htc:*
                 9: gb_est1:*
                 10: gb_est2:*
                 11: gb_htc:*
                 12: gb_est3:*
                 13: gb_est4:*
                 14: gb_est5:*
                 15: em_estfun:*
                 16: em_estom:*
                 17: em_gss_hum:*
                 18: em_gss_inv:*
                 19: em_gss_pln:*
                 20: em_gss_vrt:*
                 21: em_gss_fun:*
                 22: em_gss_mam:*
                 23: em_gss_mus:*
                 24: em_gss_pro:*
                 25: em_gss_rod:*
                 26: em_gss_phg:*
                 27: em_gss_vrl:*
                 28: gb_gss1:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	22	1.8	618	12	BG656707	BG656707 df47b06.y
c	2	22	1.8	852	14	CD252970	CD252970 AGENCOURT
c	3	21	1.7	358	29	TA58F03Q	AL455737 T. brucei
	4	21	1.7	558	28	AZ387580	AZ387580 1M0147G09
c	5	20	1.7	479	28	AZ552929	AZ552929 RPCI-23-1
c	6	20	1.7	636	28	AZ241095	AZ241095 RPCI-23-3
	7	20	1.7	794	9	AI439244	AI439244 ti59a03.x
	8	20	1.7	971	12	BG393115	BG393115 602411384
	9	19	1.6	285	28	CC112112	CC112112 NDL.23C11
	10	19	1.6	290	28	CC142352	CC142352 NDL.69F6.
c	11	19	1.6	300	9	AU231710	AU231710 AU231710
	12	19	1.6	308	28	CC013856	CC013856 PUEBF69TD
	13	19	1.6	317	10	BE364026	BE364026 PI1_11_F0
c	14	19	1.6	380	14	CD814439	CD814439 BN15.023B
	15	19	1.6	380	28	BH877108	BH877108 hr35e11.b
	16	19	1.6	387	28	BZ331847	BZ331847 hx23d03.g
	17	19	1.6	411	28	BZ648869	BZ648869 OGAOP23TC
	18	19	1.6	419	12	BP099919	BP099919 BP099919
c	19	19	1.6	428	28	BZ346375	BZ346375 hv18b09.b
	20	19	1.6	442	14	CD003371	CD003371 EST1504 N
c	21	19	1.6	445	28	BH127538	BH127538 G-1h21.f
	22	19	1.6	452	28	BH710348	BH710348 BOMBV59TF
	23	19	1.6	460	28	AZ696294	AZ696294 RPCI-23-2
	24	19	1.6	465	28	BH869577	BH869577 hl45f07.g
	25	19	1.6	478	12	BI419494	BI419494 LjNEST40f
	26	19	1.6	478	14	CF053940	CF053940 QCN22g05.
c	27	19	1.6	486	28	AQ934851	AQ934851 RPCI-23-2
	28	19	1.6	490	28	CC156727	CC156727 ig15b10.b
	29	19	1.6	502	13	BQ533490	BQ533490 LEAF4_22_
	30	19	1.6	503	28	BZ315255	BZ315255 ia56f04.b
	31	19	1.6	524	28	BZ333551	BZ333551 hx70h12.g
c	32	19	1.6	527	13	BQ588119	BQ588119 E012337-0
	33	19	1.6	539	28	CC166564	CC166564 ii54h04.b
	34	19	1.6	547	28	BZ309344	BZ309344 ic06a10.b
	35	19	1.6	556	29	PT022K05R	AL446773 Parameciu
c	36	19	1.6	559	29	CNS02DIZ	AL192500 Tetraodon
	37	19	1.6	560	28	BZ336835	BZ336835 hz39e06.b
	38	19	1.6	561	28	BZ628389	BZ628389 ih59h05.g
	39	19	1.6	578	28	BZ305613	BZ305613 hw56b06.b
	40	19	1.6	584	13	CA035588	CA035588 4001314 B
c	41	19	1.6	585	28	BZ165599	BZ165599 CH230-277
c	42	19	1.6	588	28	BZ648875	BZ648875 OGAOP23TM
c	43	19	1.6	589	28	BZ331908	BZ331908 hx23h11.g
c	44	19	1.6	590	28	AQ753987	AQ753987 HS_5395_B
c	45	19	1.6	591	29	PT017E15U	AL447151 Parameciu

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 11:03:58 ; Search time 2848 Seconds
                                          (without alignments)
                                          3409.003 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTGCVPQPA.........ALLHADFFGPEDGSIQCESN 224

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083425_11920/app_query.fasta_1
.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_@CGN_1_1_4958_@runat_30042004_083425_11920 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   GenEmbl:*
                 1: gb_ba:*
                 2: gb_htg:*
                 3: gb_in:*
                 4: gb_om:*
                 5: gb_ov:*
                 6: gb_pat:*
                 7: gb_ph:*
                 8: gb_pl:*
                 9: gb_pr:*
                 10: gb_ro:*

```
11:  gb_sts:*
12:  gb_sy:*
13:  gb_un:*
14:  gb_vi:*
15:  em_ba:*
16:  em_fun:*
17:  em_hum:*
18:  em_in:*
19:  em_mu:*
20:  em_om:*
21:  em_or:*
22:  em_ov:*
23:  em_pat:*
24:  em_ph:*
25:  em_pl:*
26:  em_ro:*
27:  em_sts:*
28:  em_un:*
29:  em_vi:*
30:  em_htg_hum:*
31:  em_htg_inv:*
32:  em_htg_other:*
33:  em_htg_mus:*
34:  em_htg_pln:*
35:  em_htg_rod:*
36:  em_htg_mam:*
37:  em_htg_vrt:*
38:  em_sy:*
39:  em_htgo_hum:*
40:  em_htgo_mus:*
41:  em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1159	100.0	1211	6	AX394331	AX394331 Sequence
	2	1159	100.0	309400	6	AX127153	AX127153 Sequence
	3	1159	100.0	325651	1	AP005283	AP005283 Corynebac
	4	1037	89.5	603	6	AX123500	AX123500 Sequence
	5	1037	89.5	603	6	BD165617	BD165617 Novel pol
	6	652	56.3	87340	1	AP005224	AP005224 Corynebac
	7	348.5	30.1	53793	1	BX248361	BX248361 Corynebac
	8	282.5	24.4	278492	1	BX248347	BX248347 Mycobacte
	9	280.5	24.2	14563	1	AE007193	AE007193 Mycobacte
	10	272.5	23.5	244800	1	BX842584	BX842584 Mycobacte
c	11	264.5	22.8	35336	1	MSGY367	AD000008 Mycobacte
c	12	253	21.8	303550	1	SCO939118	AL939118 Streptomy
	13	249.5	21.5	300425	1	AP005038	AP005038 Streptomy
	14	245	21.1	4026	1	SCO007313	AJ007313 Streptomy
c	15	242	20.9	1185	6	AX123502	AX123502 Sequence
c	16	242	20.9	1185	6	BD165619	BD165619 Novel pol

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OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 11:02:03 ; Search time 345 Seconds
                                         (without alignments)
                                         2758.250 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTGCVPQPA..........ALLHADFFGPEDGSIQCESN 224

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083424_11908/app_query.fasta_1
.391
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_@CGN_1_1_885_@runat_30042004_083424_11908 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   N_Geneseq_29Jan04:*
                 1: geneseqn1980s:*
                 2: geneseqn1990s:*
                 3: geneseqn2000s:*
                 4: geneseqn2001as:*
                 5: geneseqn2001bs:*
                 6: geneseqn2002s:*
                 7: geneseqn2003as:*
                 8: geneseqn2003bs:*
                 9: geneseqn2003cs:*
                 10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	1159	100.0	1211	6	AAL42355	Aal42355 Corynebac
	2	1159	100.0	309400	5	AAH68534	Aah68534 C glutami
	3	1037	89.5	603	5	AAH68381	Aah68381 C glutami
	4	1037	89.5	603	7	ACA01297	Aca01297 C. glutam
	5	280.5	24.2	103765	4	AAI99683_43	Continuation (44 o
	6	272.5	23.5	11529	4	AAI99682_44	Continuation (45 o
	7	272.5	23.5	110000	4	AAI99682_43	Continuation (44 o
c	8	242	20.9	1185	5	AAH68383	Aah68383 C glutami
	9	221.5	19.1	639	5	AAH66206	Aah66206 C glutami
	10	221.5	19.1	648	7	ACA00415	Aca00415 C. glutam
	11	221.5	19.1	1330	6	AAD35114	Aad35114 Corynebac
	12	221.5	19.1	2086	6	AAD35115	Aad35115 Corynebac
	13	221.5	19.1	349980	5	AAH68527	Aah68527 C glutami
	14	211.5	18.2	647	2	AAQ70249	Aaq70249 P. aerugi
	15	211.5	18.2	647	2	AAQ70242	Aaq70242 P. aerugi
	16	211.5	18.2	647	3	AAA51919	Aaa51919 P. aerugi
	17	205	17.7	570	7	ACF71991	Acf71991 Photorhab
	18	205	17.7	110000	7	ACF67367_51	Continuation (52 o
	19	205	17.7	110000	7	ACF67367_52	Continuation (53 o
	20	205	17.7	110000	7	ACF65387_3	Continuation (4 of
	21	201	17.3	110000	2	AAT42063_06	Continuation (7 of
	22	194	16.7	771	6	ABT05614	Abt05614 Mycobacte
	23	194	16.7	771	7	ABZ71111	Abz71111 Mycobacte
	24	194	16.7	75216	6	ABX09141	Abx09141 Mycobacte
	25	194	16.7	110000	4	AAI99682_13	Continuation (14 o
	26	194	16.7	110000	4	AAI99683_13	Continuation (14 o
	27	193.5	16.7	38675	9	ADB74386	Adb74386 Mycobacte
c	28	178	15.4	14615	4	AAS59577	Aas59577 Propionib
c	29	178	15.4	14615	7	ACF64506	Acf64506 Propionib
	30	169.5	14.6	579	5	AAH65249	Aah65249 C glutami
	31	169.5	14.6	579	7	ACA01964	Aca01964 C. glutam
	32	169.5	14.6	1109	6	AAD33874	Aad33874 Corynebac
c	33	169.5	14.6	349980	5	AAH64966	Aah64966 C glutami
	34	164.5	14.2	564	6	ABK74063	Abk74063 Bacillus
	35	160.5	13.8	603	3	AAA64868	Aaa64868 Bordetell
c	36	160.5	13.8	35026	3	AAA64890	Aaa64890 Bordetell
c	37	153.5	13.2	747	7	ACF65615	Acf65615 Photorhab
	38	153	13.2	651	3	AAA39563	Aaa39563 M. tuberc
c	39	153	13.2	110000	4	AAI99682_35	Continuation (36 o
c	40	153	13.2	110000	4	AAI99683_35	Continuation (36 o
	41	146.5	12.6	37856	3	AAA11992	Aaa11992 S. cellul
	42	144	12.4	110000	4	AAI99682_23	Continuation (24 o
	43	144	12.4	110000	4	AAI99683_23	Continuation (24 o
c	44	142.5	12.3	735	7	ACF65674	Acf65674 Photorhab
c	45	140	12.1	110000	4	AAI99682_37	Continuation (38 o

ALIGNMENTS

```
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OM protein - nucleic search, using frame_plus_p2n model

Run on:          May  1, 2004, 12:09:03 ; Search time 85 Seconds
                                          (without alignments)
                                          1462.459 Million cell updates/sec

Title:           US-09-942-935-2
Perfect score:   1159
Sequence:        1 MENLPILSRIRDTGCVPQPA..........ALLHADFFGPEDGSIQCESN 224

Scoring table:   BLOSUM62
                 Xgapop 10.0 , Xgapext  0.5
                 Ygapop 10.0 , Ygapext  0.5
                 Fgapop  6.0 , Fgapext  7.0
                 Delop   6.0 , Delext   7.0

Searched:        682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters:       1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083426_11947/app_query.fasta_1
.391
-DB=Issued_Patents_NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09942935_@CGN_1_1_103_@runat_30042004_083426_11947 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :       Issued_Patents_NA:*
                 1:  /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
                 2:  /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
                 3:  /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
                 4:  /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
                 5:  /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
                 6:  /cgn2_6/ptodata/2/ina/backfiles1.seq:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.
```

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	280.5	24.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
	2	272.5	23.5	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	3	211.5	18.2	647	1	US-08-260-202A-9	Sequence 9, Appli
	4	211.5	18.2	647	1	US-08-017-114-9	Sequence 9, Appli
	5	211.5	18.2	647	3	US-08-505-307-9	Sequence 9, Appli
	6	211.5	18.2	647	4	US-09-609-151A-9	Sequence 9, Appli
	7	211.5	18.2	647	5	PCT-US94-02034-9	Sequence 9, Appli
	8	211.5	18.2	840	4	US-09-252-991A-13069	Sequence 13069, A
	9	201	17.3	1830121	4	US-09-557-884-1	Sequence 1, Appli
	10	201	17.3	1830121	4	US-09-643-990A-1	Sequence 1, Appli
	11	193.5	16.7	615	4	US-09-489-039A-4559	Sequence 4559, Ap
	12	193.5	16.7	38675	4	US-08-311-731A-135	Sequence 135, App
	13	188	16.2	600	4	US-09-543-681A-3510	Sequence 3510, Ap
c	14	153	13.2	4403765	3	US-09-103-840A-2	Sequence 2, Appli
c	15	153	13.2	4411529	3	US-09-103-840A-1	Sequence 1, Appli
	16	141.5	12.2	846	4	US-09-252-991A-9635	Sequence 9635, Ap
c	17	141.5	12.2	1062	4	US-09-252-991A-9532	Sequence 9532, Ap
	18	141.5	12.2	1371	4	US-09-252-991A-9717	Sequence 9717, Ap
c	19	132	11.4	6464	4	US-09-221-017B-168	Sequence 168, App
	20	128	11.0	540	4	US-09-134-000C-1484	Sequence 1484, Ap
	21	127	11.0	603	4	US-09-134-000C-797	Sequence 797, App
c	22	124	10.7	9837	4	US-09-221-017B-636	Sequence 636, App
	23	112	9.7	597	4	US-09-252-991A-13522	Sequence 13522, A
	24	106.5	9.2	525	4	US-09-107-532A-1956	Sequence 1956, Ap
	25	106.5	9.2	621	4	US-09-252-991A-1369	Sequence 1369, Ap
c	26	105	9.1	1239	4	US-09-252-991A-12715	Sequence 12715, A
c	27	103.5	8.9	1753	4	US-09-221-017B-1063	Sequence 1063, Ap
c	28	102	8.8	1524	4	US-09-252-991A-1651	Sequence 1651, Ap
	29	102	8.8	1770	4	US-09-252-991A-1522	Sequence 1522, Ap
	30	99.5	8.6	717	4	US-09-328-352-2206	Sequence 2206, Ap
c	31	99	8.5	129908	4	US-09-585-858-1	Sequence 1, Appli
c	32	98.5	8.5	894	4	US-09-252-991A-1599	Sequence 1599, Ap
	33	89	7.7	819	4	US-09-252-991A-11741	Sequence 11741, A
c	34	89	7.7	1686	4	US-09-252-991A-11503	Sequence 11503, A
	35	89	7.7	1920	4	US-09-252-991A-11882	Sequence 11882, A
c	36	88	7.6	1872	4	US-09-252-991A-6335	Sequence 6335, Ap
	37	88	7.6	2112	4	US-09-252-991A-6212	Sequence 6212, Ap
	38	87.5	7.5	1553	4	US-09-620-312D-490	Sequence 490, App
	39	86	7.4	1548	2	US-08-762-106-5	Sequence 5, Appli
	40	86	7.4	1548	3	US-09-320-774-5	Sequence 5, Appli
	41	85.5	7.4	1497	4	US-09-489-039A-6536	Sequence 6536, Ap
	42	84.5	7.3	2220	4	US-09-540-236-863	Sequence 863, App
c	43	84.5	7.3	94750	4	US-09-596-002-38	Sequence 38, Appl
	44	84	7.2	1758	4	US-09-252-991A-490	Sequence 490, App
c	45	84	7.2	1794	4	US-09-252-991A-568	Sequence 568, App

ALIGNMENTS

RESULT 1
US-09-103-840A-2
; Sequence 2, Application US/09103840A

OM protein - nucleic search, using frame_plus_p2n model

Run on: May 1, 2004, 13:19:54 ; Search time 357 Seconds
                                          (without alignments)
                                          2838.252 Million cell updates/sec

Title: US-09-942-935-2
Perfect score: 1159
Sequence: 1 MENLPILSRIRDTGCVPQPA.........ALLHADFFGPEDGSIQCESN 224

Scoring table: BLOSUM62
                 Xgapop 10.0 , Xgapext 0.5
                 Ygapop 10.0 , Ygapext 0.5
                 Fgapop 6.0 , Fgapext 7.0
                 Delop   6.0 , Delext   7.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-
Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083427_12038/app_query.fasta_1
.391
-DB=Published_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USER=US09942935_@CGN_1_1_107_@runat_30042004_083427_12038
-NCPU=6 -ICPU=3 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :   Published_Applications_NA:*
                 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
                 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
                 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
                 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
                 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
                 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
                 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
                 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
                 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
                 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

```
12:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
13:  /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
14:  /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
15:  /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16:  /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17:  /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18:  /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19:  /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1159	100.0	1211	9	US-09-942-935-1	Sequence 1, Appli
2	1159	100.0	3309400	9	US-09-738-626-1	Sequence 1, Appli
3	1037	89.5	603	9	US-09-738-626-3416	Sequence 3416, Ap
4	249.5	21.5	711	15	US-10-156-761-4287	Sequence 4287, Ap
5	249.5	21.5	9025608	15	US-10-156-761-1	Sequence 1, Appli
c 6	242	20.9	1185	9	US-09-738-626-3418	Sequence 3418, Ap
7	221.5	19.1	639	9	US-09-738-626-1241	Sequence 1241, Ap
8	221.5	19.1	1330	9	US-09-935-757-1	Sequence 1, Appli
9	221.5	19.1	2086	9	US-09-935-757-5	Sequence 5, Appli
c 10	201.5	17.4	9025608	15	US-10-156-761-1	Sequence 1, Appli
11	201	17.3	1830121	15	US-10-329-960-1	Sequence 1, Appli
12	201	17.3	1830121	16	US-10-329-670-1	Sequence 1, Appli
13	198	17.1	657	15	US-10-156-761-3104	Sequence 3104, Ap
14	194	16.7	75216	15	US-10-080-170-646	Sequence 646, App
15	182.5	15.7	681	15	US-10-156-761-3025	Sequence 3025, Ap
16	169.5	14.6	579	9	US-09-738-626-284	Sequence 284, App
17	169.5	14.6	1109	9	US-09-941-936A-1	Sequence 1, Appli
c 18	169.5	14.6	3309400	9	US-09-738-626-1	Sequence 1, Appli
19	164.5	14.2	564	9	US-09-974-300-1354	Sequence 1354, Ap
20	150.5	13.0	594	15	US-10-156-761-5107	Sequence 5107, Ap
21	149	12.9	612	15	US-10-156-761-886	Sequence 886, App
22	147.5	12.7	618	15	US-10-156-761-6054	Sequence 6054, Ap
23	145	12.5	651	15	US-10-156-761-606	Sequence 606, App
24	137.5	11.9	618	9	US-09-738-626-855	Sequence 855, App
25	137.5	11.9	1148	9	US-09-942-936-1	Sequence 1, Appli
26	135	11.6	546	13	US-10-282-122A-12529	Sequence 12529, A
27	134	11.6	576	15	US-10-156-761-3305	Sequence 3305, Ap
28	132.5	11.4	537	15	US-10-156-761-4690	Sequence 4690, Ap
c 29	132	11.4	6464	13	US-10-194-163-168	Sequence 168, App
30	130.5	11.3	577	9	US-09-974-300-1365	Sequence 1365, Ap
31	130	11.2	1002	15	US-10-156-761-3350	Sequence 3350, Ap
32	129.5	11.2	526	9	US-09-974-300-1380	Sequence 1380, Ap
33	129.5	11.2	537	15	US-10-156-761-4048	Sequence 4048, Ap
34	129.5	11.2	540	9	US-09-974-300-5795	Sequence 5795, Ap
35	129.5	11.2	546	15	US-10-156-761-7271	Sequence 7271, Ap
36	128	11.0	24601	9	US-09-070-927A-223	Sequence 223, App
c 37	127	11.0	10636	9	US-09-070-927A-74	Sequence 74, Appl
38	125.5	10.8	612	15	US-10-156-761-1204	Sequence 1204, Ap
39	125	10.8	618	15	US-10-156-761-3338	Sequence 3338, Ap

```
                        GenCore version 5.1.6
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  OM protein - nucleic search, using frame_plus_p2n model

  Run on:          May  1, 2004, 12:06:28 ; Search time 2506 Seconds
                                           (without alignments)
                                           2669.245 Million cell updates/sec

  Title:           US-09-942-935-2
  Perfect score:   1159
  Sequence:        1 MENLPILSRIRDTGCVPQPA..........ALLHADFFGPEDGSIQCESN 224

  Scoring table:   BLOSUM62
                   Xgapop 10.0 , Xgapext  0.5
                   Ygapop 10.0 , Ygapext  0.5
                   Fgapop  6.0 , Fgapext  7.0
                   Delop   6.0 , Delext   7.0

  Searched:        27513289 seqs, 14931090276 residues

  Total number of hits satisfying chosen parameters:      55026578

  Minimum DB seq length: 0
  Maximum DB seq length: 2000000000

  Post-processing: Minimum Match 0%
                   Maximum Match 100%
                   Listing first 45 summaries

  Command line parameters:
  -MODEL=frame+_p2n.model -DEV=xlp
  -
  Q=/cgn2_1/USPTO_spool_p/US09942935/runat_30042004_083425_11934/app_query.fasta_1
  .391
  -DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
  -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
  -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
  -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
  -USER=US09942935_@CGN_1_1_3549_@runat_30042004_083425_11934 -NCPU=6 -ICPU=3
  -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
  -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
  -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

  Database :       EST:*
                   1:  em_estba:*
                   2:  em_esthum:*
                   3:  em_estin:*
                   4:  em_estmu:*
                   5:  em_estov:*
                   6:  em_estpl:*
                   7:  em_estro:*
                   8:  em_htc:*
                   9:  gb_est1:*
                   10:  gb_est2:*
                   11:  gb_htc:*
```

```
12:  gb_est3:*
13:  gb_est4:*
14:  gb_est5:*
15:  em_estfun:*
16:  em_estom:*
17:  em_gss_hum:*
18:  em_gss_inv:*
19:  em_gss_pln:*
20:  em_gss_vrt:*
21:  em_gss_fun:*
22:  em_gss_mam:*
23:  em_gss_mus:*
24:  em_gss_pro:*
25:  em_gss_rod:*
26:  em_gss_phg:*
27:  em_gss_vrl:*
28:  gb_gss1:*
29:  gb_gss2:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	174	15.0	879	11	BC022210	BC022210 Homo sapi
c	2	154.5	13.3	761	28	BH242195	BH242195 ATZFD48TF
	3	148	12.8	893	13	BQ931778	BQ931778 AGENCOURT
	4	146.5	12.6	968	28	BZ561490	BZ561490 pacs2-164
	5	139	12.0	321	13	BU275590	BU275590 Cr_Emb_04
c	6	130	11.2	943	28	BZ552424	BZ552424 pacs1-60_
	7	117.5	10.1	542	28	BH823104	BH823104 BACPP18-H
	8	117.5	10.1	626	28	BH832826	BH832826 BACPP4-G1
c	9	116	10.0	573	28	BH391760	BH391760 AG-ND-148
c	10	111	9.6	436	28	BH403298	BH403298 AG-ND-132
c	11	111	9.6	742	28	BH393492	BH393492 AG-ND-138
	12	109.5	9.4	804	28	BH242457	BH242457 ATZFC44TF
c	13	109.5	9.4	1844	28	BH614306	BH614306 1C22/2B8_
c	14	109.5	9.4	1844	28	BH614501	BH614501 2B8_Conti
c	15	109	9.4	456	28	BH374042	BH374042 AG-ND-143
c	16	105.5	9.1	375	28	AZ576920	AZ576920 03a11 Sho
	17	105	9.1	1052	13	BU857304	BU857304 AGENCOURT
	18	104	9.0	872	28	BH372133	BH372133 AG-ND-133
	19	102.5	8.8	768	14	CK029060	CK029060 AGENCOURT
	20	102.5	8.8	793	14	CF347223	CF347223 AGENCOURT
	21	102.5	8.8	1083	14	CB923509	CB923509 STR00853
c	22	102	8.8	1012	28	BZ573065	BZ573065 msh2_2928
c	23	101.5	8.8	698	14	CB851398	CB851398 UI-CF-DU1
c	24	101.5	8.8	797	14	CF891232	CF891232 UI-CF-DU1
c	25	101	8.7	768	28	BZ675390	BZ675390 PUBKV84TD
	26	101	8.7	795	12	BI704389	BI704389 zfshTARAM
	27	100.5	8.7	2321	11	AY108097	AY108097 Zea mays
	28	97.5	8.4	713	13	BQ616834	BQ616834 faa95g01.
	29	97	8.4	683	13	BX847466	BX847466 BX847466